Amendment to the Claims:

Please amend the claims as follows:

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claims 1 to 30 (canceled)

Claim 31 (previously presented) A method of producing a polypeptide polymer comprising the steps of:

(a) providing a plurality of monomeric polypeptides and at least one divalent cation, wherein the monomer polypeptides are capable of self-assembly in the presence of a divalent cation; and

(b) (i) polymerizing the monomeric polypeptides through a self-assembly process in the presence of at least one divalent cation, or, (ii) polymerizing the monomeric polypeptides in the presence of a template molecule.

Claim 32 (currently amended): The method of claim 31, wherein the monomeric polypeptide has an amino acid sequence as set forth in SEQ ID NO:2, ~~SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, or SEQ ID NO:10, wherein~~ and the amino acid sequence has at least one conservative substitution and the polypeptide with the conservative substitution can self-assemble to form a polymer .

Claim 33 (currently amended): The method of claim 31, wherein [[the]] at least one monomeric polypeptide is encoded by a nucleic acid comprising a sequence having at least about 50% sequence identity with a nucleic acid sequence as set forth in SEQ ID NO:1, ~~SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, or SEQ ID NO:9,~~ over a subsequence of at least about 100 residues.

Claim 34 (currently amended): The method of claim 31, wherein the step of providing a plurality of monomeric polypeptides further comprises the steps of:

preparing a vector comprising a nucleic acid, wherein the nucleic acid encodes the polypeptide;

inserting the vector into a host cell;

growing the host cell in a suitable culture to express the nucleic acid to form the polypeptide; and

isolating the formed monomeric polypeptide from the host cell.

Claim 35 (currently amended): The method of claim 31, wherein the step of polymerizing the monomeric polypeptides further comprises the steps of:

dissolving the plurality of monomeric polypeptides in a solution; and

adding a template molecule and an alkaline earth metal ion to the solution.

Claim 36 (previously presented): The method of claim 34, wherein the vector comprises plasmid pEX-CAN-A.

Claim 37 (previously presented): The method of claim 36, wherein the host cell comprises a host cell selected from the group consisting of an *E. coli* (DE3) and a *Pseudomonas*.

Claims 38 to 40 (canceled)

Claim 41 (currently amended): A method of encapsulating a molecule comprising the steps of:

providing a solution of a plurality of polypeptides having an amino acid sequence as set forth in SEQ ID NO:2, ~~SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, or SEQ ID NO:10,~~ wherein the amino acid sequence has at least one conservative substitution and the polypeptides can self-assemble to form a polymer and

polymerizing the plurality of polypeptides the presence of the molecule so as to encapsulate the molecule in the polymer.

Claim 42 (currently amended): The method of claim 41, wherein the solution of polypeptides provided further comprises at least one polypeptide comprising ~~of said polypeptides comprises~~ a sequence as set forth in [[SEQ ID NO:2,]] SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, or SEQ ID NO:10.

Claim 43 to 113 (canceled)

Claim 114 (previously presented): The method of claim 34, wherein the vector is selected from the group consisting of viral vectors, plasmid vectors, phage vectors, phagemid vectors, cosmids, fosmids, bacteriophages, artificial chromosomes, adenovirus vectors, retroviral vectors, and adeno-associated vectors.

Claim 115 (previously presented): The method of claim 34, wherein the host is selected from the group consisting of prokaryotes, eukaryotes, funguses, yeasts, plants and metabolically rich hosts.

Claims 116 to 131 (canceled)

Claim 132 (previously presented): The method of claim 31, wherein the monomeric polypeptides have a molecular weight of more than 5,000 daltons.

Claim 133 (previously presented): The method of claim 132, wherein the monomeric polypeptides have a molecular weight of more than 10,000 daltons.

Claim 134 (previously presented): The method of claim 31, wherein the monomeric polypeptides polymerize to form a hollow tube, a tubule, a micelle or a molecular sieve.

Claim 135 (previously presented): The method of claim 134, wherein the hollow tube has approximately a 25 nm outer diameter and a 20 nm inner diameter.

Claim 136 (previously presented): The method of claim 31, wherein the monomeric polypeptides are polymerized in the presence of a divalent cation and a template molecule.

Claim 137 (previously presented): The method of claim 31, wherein the template molecule comprises a plasmid, a phage, a cosmid, a phagemid, a virus or a portion of a virus.

Claim 138 (previously presented): The method of claim 137, wherein the virus comprises a retrovirus, a parainfluenzavirus, a herpesvirus, a reovirus or a paramyxovirus.

Claim 139 (previously presented): The method of claim 137, wherein the portion of a virus comprises a coat protein, a spike glycoprotein or a capsid protein.

Claim 140 (previously presented): The method of claim 31, wherein the plurality of monomeric polypeptides are polymerized in the presence of at least one divalent cation selected from the group consisting of Ca^{2+}, Mg^{2+}, Cu^{2+}, Zn^{2+}, Sr^{2+}, Ni^{2+}, Mn^{2+} and Fe^{2+}.

Claim 141 (previously presented): The method of claim 31, wherein the plurality of monomeric polypeptides are polymerized in the presence of Ca^{2+} and Mg^{2+}.

Claim 142 (previously presented): The method of claim 31, wherein the step of polymerizing the monomeric polypeptides further comprises the step of dissolving the monomeric polypeptides in an aqueous solution.

Claim 143 (previously presented): The method of claim 31, wherein the template molecule is prepared by fragmenting or shearing of a suspension of a polymer.

Claim 144 (previously presented): The method of claim 31, wherein the monomeric polypeptides or polymers interact with each other by pairing, bundling, entangling or

electrostatic cross-linking, thereby generating paired polymers, bundled polymers, entangled polymers, cross-linked polymers or an interconnected network of polymers.

Claim 145 (previously presented): The method of claim 31, further comprising providing a therapeutic agent or a drug molecule and adding the therapeutic agent or drug molecule to the polymerization step, thereby generating a therapeutic agent or drug molecule encapsulated by the polymers.

Claim 146 (previously presented): The method of claim 145, wherein the therapeutic agent or drug molecule is added to the polymerization step when a partially formed polymer is formed.

Claim 147 (previously presented): The method of claim 146, further comprising capping the partially formed polymer using a capping unit.

Claim 148 (previously presented): The method of claim 147, wherein the capping unit comprises a polypeptide monomer.

Claim 149 (previously presented): The method of claim 146, wherein the therapeutic agent or drug encapsulating step is carried out by mixing the polymer and the therapeutic agent or drug molecule together in a solution such that the therapeutic agent or drug molecule can permeate inside the polymer.

Claim 150 (previously presented): The method of claim 145, further comprising attaching a targeting molecule or a vector to the therapeutic agent- or drug-loaded polymer during the encapsulation process or after the completion of the encapsulation process.

Claim 151 (previously presented): The method of claim 145, further comprising using lipids or lipid molecules during the encapsulation process.

Claim 152 (previously presented): The method of claim 151, wherein liposomes are induced to form from the lipids in the presence of both the therapeutic agent or drug molecules and the monomeric polypeptides.

Claim 152 (previously presented): The method of claim 31, further comprising attaching the polymer to a hydrogel.

Claim 153 (previously presented): The method of claim 152, wherein the hydrogel comprises a three-dimensional structural network for a biochip.

Claim 154 (currently amended): The method of claim [[32]] 31, wherein the monomeric polypeptide has an amino acid sequence as set forth in SEQ ID NO:2~~, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, or SEQ ID NO:10~~.

Claim 155 (currently amended): The method of claim 31, wherein [[the]] at least one monomeric polypeptide has an amino acid sequence having at least 50% sequence identity to an amino acid sequence as set forth in SEQ ID NO:2~~, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, or SEQ ID NO:10~~ over at least about 40 consecutive amino acid residues.

Claim 156 (previously presented): The method of claim 155, wherein the sequence identity is at least 55%.

Claim 157 (previously presented): The method of claim 156, wherein the sequence identity is at least 60%.

Claim 158 (previously presented): The method of claim 157, wherein the sequence identity is at least 65%.

Claim 159 (previously presented): The method of claim 158, wherein the sequence identity is at least 70%.

Claim 160 (previously presented): The method of claim 159, wherein the sequence identity is at least 75%.

Claim 161 (previously presented): The method of claim 160, wherein the sequence identity is at least 80%.

Claim 162 (previously presented): The method of claim 161, wherein the sequence identity is at least 85%.

Claim 163 (previously presented): The method of claim 162, wherein the sequence identity is at least 90%.

Claim 164 (previously presented): The method of claim 163, wherein the sequence identity is at least 95%.

Claim 165 (previously presented): The method of claim 164, wherein the sequence identity is at least 97%.

Claim 166 (previously presented): The method of claim 155, wherein the sequence identity is over at least about 50 consecutive amino acid residues.

Claim 167 (previously presented): The method of claim 166, wherein the sequence identity is over at least about 75 consecutive amino acid residues.

Claim 168 (previously presented): The method of claim 167, wherein the sequence identity is over at least about 100 consecutive amino acid residues.

Claim 169 (previously presented): The method of claim 168, wherein the sequence identity is over at least about 150 consecutive amino acid residues.

Claim 170 (previously presented): The method of claim 169, wherein the sequence identity is over the full length of the polypeptide.

Claim 171 (previously presented): The method of claim 33, wherein the sequence identity is at least 55%.

Claim 172 (previously presented): The method of claim 171, wherein the sequence identity is at least 60%.

Claim 173 (previously presented): The method of claim 172, wherein the sequence identity is at least 65%.

Claim 174 (previously presented): The method of claim 173, wherein the sequence identity is at least 70%.

Claim 175 (previously presented): The method of claim 174, wherein the sequence identity is at least 75%.

Claim 176 (previously presented): The method of claim 175, wherein the sequence identity is at least 80%.

Claim 177 (previously presented): The method of claim 176, wherein the sequence identity is at least 85%.

Claim 178 (previously presented): The method of claim 177, wherein the sequence identity is at least 90%.

Claim 179 (previously presented): The method of claim 178, wherein the sequence identity is at least 95%.

Claim 180 (previously presented): The method of claim 179, wherein the sequence identity is at least 97%.

Claim 181 (previously presented): The method of claim 33, wherein the sequence identity is over at least about 150 consecutive residues.

Claim 182 (previously presented): The method of claim 181, wherein the sequence identity is over at least about 200 consecutive residues.

Claim 183 (previously presented): The method of claim 182, wherein the sequence identity is over at least about 300 consecutive residues.

Claim 184 (previously presented): The method of claim 183, wherein the sequence identity is over at least about 400 consecutive residues.

Claim 185 (previously presented): The method of claim 184, wherein the sequence identity is over the full length of the nucleic acid.

Claim 186 (currently amended): The method of claim 31, wherein [[the]] at least one monomeric polypeptide is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid having a sequence as set forth in SEQ ID NO:1, ~~SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, or SEQ ID NO:9,~~ wherein the stringent conditions comprise a washing step comprising 2X SSC, 0.1% SDS at room temperature for 15 minutes.

Claim 187 (currently amended): The method of claim 31, wherein [[the]] at least one monomeric polypeptide is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid having a sequence as set forth in SEQ ID NO:1, ~~SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, or SEQ ID NO:9,~~ wherein the stringent conditions comprise a washing step comprising 0.1X SSC, 0.5% SDS at room temperature for 30 minutes to 1 hour.

Claim 188 (currently amended): The method of claim 31, wherein [[the]] at least one monomeric polypeptide is encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid having a sequence as set forth in SEQ ID NO:1, ~~SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, or SEQ ID NO:9,~~ wherein the stringent conditions comprise a washing step comprising 0.1X SSC, 0.5% SDS for 15 to 30 minutes at between the hybridization temperature and 68°C.

Claim 189 (previously presented): The method of claim 32, wherein the conservative amino acid substitution comprises substituting one amino acid for another of the same class.

Claim 190 (previously presented): The method of claim 189, wherein the conservative amino acid substitution comprises substitution of one hydrophobic amino acid for another, or, substitution of one polar amino acid for another.

Claim 191 (previously presented): The method of claim 190, wherein the conservative amino acid substitution comprises substitution of isoleucine, valine, leucine or methionine, for another hydrophobic amino acid.

Claim 192 (previously presented): The method of claim 190, wherein the conservative amino acid substitution comprises substitution of arginine for lysine, glutamic acid for aspartic acid or glutamine for asparagine.